

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANTS: Iris Pecker et al.
- (ii) TITLE OF INVENTION: HEPARANASE SPECIFIC MOLECULAR PROBES AND THEIR USE IN RESEARCH AND MEDICAL APPLICATIONS
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: G. E. Ehrlich (1995) Ltd.
c/o Anthony Castorina
2001 Jefferson Davis Highway, Suite 207
Arlington
Virginia
United States of America
22202
- (B) STREET:
- (C) CITY:
- (D) STATE:
- (E) COUNTRY:
- (F) ZIP:
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
- (B) COMPUTER: Twinhead* Slimnote-890TX
- (C) OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11
- (D) SOFTWARE: Word for Windows version 2.0 converted to an ASCII file
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/922,180
- (B) FILING DATE: September 2, 1997
- (A) APPLICATION NUMBER: 09/071,739
- (B) FILING DATE: May 1, 1998
- (A) APPLICATION NUMBER: 09/322,977
- (B) FILING DATE: June 1, 1999
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Sol Sheinbein
- (B) REGISTRATION NUMBER: 25,457
- (C) REFERENCE/DOCKET NUMBER: 00/21505
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 972-3-6127676
- (B) TELEFAX: 972-3-6127575
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1721
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

CTAGAGCTTT CGACTCTCCG CTGCGCGGGG GGTGAGCCCA GGTGAGCCCA 60
AGATGCTGCT GCCTCGAAG CCTGCGCTGC CGCGCCGCT GATGCTGCT CTCCTGGGGC 120
CGCTGGGTCC CCTCTCCCTT GCGCCCTGC CCCGACCTGC GCAAGCACAG GACGTCGTGG 180
ACCTGGACTT cTTACCCAG GAGCCGCTGC ACCTGGTGAG CCCCTCGTTC CTGTCCGTCA 240
CCATTGACGC CAACCTGGCC ACGGACCCGC GGTTCCTCAT CCTCTGGGT TCTCCAAAGC 300
TTCGTACCTT GGCAGAGGC TTGTCTCTG CGTACCTGAG GTTTGGTGGC ACCAAGACAG 360
ACTTCCTAAT TTTCGATCCC AAGAAGGAAT CAACCTTTGA AGAGAGAAGT TACTGGCAAT 420
CTCAAGTCAA CCAGGATATT TGCAAATATG GATCCATCCC TCCTGATGTG GAGGAGAAGT 480
TACGGTTGGA ATGCCCTAC CAGGAGCAAT TGCTACTCCG AGAACACTAC CAGAAAAAGT 540
TCAAGAACAG CACCTACTCA AGAAGCTCTG TAGATGTGCT ATACACTTTT GCAAAGTCTG 600
CAGGACTGGA CTGTATCTT GGCTAAATG CGTTATTAAG AACAGCAGAT TTGCAGTGGA 660
ACAGTTCTAA TGCTCAGTT CTCCTGGACT ACTGCTCTT CAAGGGGTAT AACATTTCTT 720
GGGAAGTAGG CAATGAACCT AACAGTTTCC TTAAGAAGGC TGATATTTTC ATCAATGGGT 780
CGCAGTTAGG AGAAGATTAT ATTCAATTGC ATAACTTCT AAGAAAGTCC ACCTTCAAAA 840
ATGCAAAACT CTATGGTCTT GATGTTGGTC AGCCTCGAAG AAAGACGGCT AAGATGCTGA 900
AGAGCTTCTT GAAGGCTGGT GGAGAAGTGA TTGATTCAGT TACATGGCAT CACTACTATT 960
TGAATGGACG GACTGCTACC AGGGAAGATT TTCTAAACCC TGATGTATTG GACATTTTTA 1020
TTTCATCTGT GCAAAAAGTT TTCCAGGTGG TTGAGAGCAC CAGGCCTGGC AAGAAGGTCT 1080
GGTTAGGAGA AACAAGCTCT GCATATGGAG GCGGAGCGCC CTTGCTATCC GACACCTTTG 1140
CAGCTGGCTT TATGTGGCTG GATAAATTGG GCCTGTCAGC CCGAATGGGA ATAGAAGTGG 1200
TGATGAGGCA AGTATTCTTT GGAGCAGGAA ACTACCATTT AGTGGATGAA AACTTCGATC 1260
CTTTACCTGA TTATTGGCTA TCCTTCTGT TCAAGAAATT GGTGGGCACC AAGGTGTTAA 1320
TGGCAAGCGT GCAAGGTTCA AAGAGAAGGA AGCTTCGAGT ATACCTTCAT TGCACAAACA 1380
CTGACAATCC AAGGTATAAA GAAGGAGATT TAACTCTGTA TGCCATAAAC CTCCATAACG 1440
TCACCAAGTA CTGCGGTTA CCCTATCTTT TTCTAACAA GCAAGTGGAT AAATACCTTC 1500
TAAGACCTTT GGGACCTCAT GGATTACTTT CCAAATCTGT CCAACTCAAT GGTCTAACTC 1560
TAAAGATGGT GGATGATCAA ACCTTGCCAC CTTTAATGGA AAAACCTCTC CGGCCAGGAA 1620
GTTCACTGGG CTGCCAGCT TTCTCATATA GTTTTTTGT GATAAGAAAT GCCAAAGTTG 1680
CTGCTTGCAT CTGAAAAATA AATATACTAG TCCTGACACT G 1721

```

(2) INFORMATION FOR SEQ ID NO:2:

[illegible]

Met	Leu	Leu	Arg	Ser 5	Lys	Pro	Ala	Leu	Pro 10	Pro	Pro	Leu	Met	Leu 15	Leu
Leu	Leu	Gly	Pro 20	Leu	Gly	Pro	Leu	Ser 25	Pro	Gly	Ala	Leu	Pro 30	Arg	Pro
Ala	Gln	Ala 35	Gln	Asp	Val	Val	Asp 40	Leu	Asp	Phe	Phe	Thr 45	Gln	Glu	Pro
Leu	His 50	Leu	Val	Ser	Pro	Ser 55	Phe	Leu	Ser	Val	Thr 60	Ile	Asp	Ala	Asn
Leu 65	Ala	Thr	Asp	Pro	Arg 70	Phe	Leu	Ile	Leu	Leu 75	Gly	Ser	Pro	Lys	Leu 80
Arg	Thr	Leu	Ala	Arg 85	Gly	Leu	Ser	Pro	Ala 90	Tyr	Leu	Arg	Phe	Gly 95	Gly
Thr	Lys	Thr	Asp 100	Phe	Leu	Ile	Phe	Asp 105	Pro	Lys	Lys	Glu	Ser 110	Thr	Phe
Glu	Glu	Arg 115	Ser	Tyr	Trp	Gln	Ser 120	Gln	Val	Asn	Gln	Asp 125	Ile	Cys	Lys
Tyr	Gly 130	Ser	Ile	Pro	Pro	Asp 135	Val	Glu	Glu	Lys	Leu 140	Arg	Leu	Glu	Trp
Pro 145	Tyr	Gln	Glu	Gln	Leu 150	Leu	Leu	Arg	Glu	His 155	Tyr	Gln	Lys	Lys	Phe 160
Lys	Asn	Ser	Thr	Tyr 165	Ser	Arg	Ser	Ser	Val 170	Asp	Val	Leu	Tyr	Thr 175	Phe
Ala	Asn	Cys	Ser 180	Gly	Leu	Asp	Leu	Ile 185	Phe	Gly	Leu	Asn	Ala 190	Leu	Leu
Arg	Thr	Ala 195	Asp	Leu	Gln	Trp	Asn 200	Ser	Ser	Asn	Ala	Gln 205	Leu	Leu	Leu
Asp	Tyr 210	Cys	Ser	Ser	Lys	Gly 215	Tyr	Asn	Ile	Ser	Trp 220	Glu	Leu	Gly	Asn
Glu 225	Pro	Asn	Ser	Phe	Leu 230	Lys	Lys	Ala	Asp	Ile 235	Phe	Ile	Asn	Gly	Ser 240
Gln	Leu	Gly	Glu	Asp 245	Tyr	Ile	Gln	Leu	His 250	Lys	Leu	Leu	Arg	Lys 255	Ser
Thr	Phe	Lys	Asn 260	Ala	Lys	Leu	Tyr	Gly 265	Pro	Asp	Val	Gly 270	Gln	Pro	Arg
Arg	Lys	Thr 275	Ala	Lys	Met	Leu	Lys 280	Ser	Phe	Leu	Lys	Ala 285	Gly	Gly	Glu
Val	Ile 290	Asp	Ser	Val	Thr	Trp 295	His	His	Tyr	Tyr	Leu 300	Asn	Gly	Arg	Thr
Ala 305	Thr	Arg	Glu	Asp	Phe 310	Leu	Asn	Pro	Asp	Val 315	Leu	Asp	Ile	Phe	Ile 320
Ser	Ser	Val	Gln	Lys 325	Val	Phe	Gln	Val	Val 330	Glu	Ser	Thr	Arg	Pro 335	Gly
Lys	Lys	Val 340	Trp	Leu	Gly	Glu	Thr	Ser 345	Ser	Ala	Tyr	Gly 350	Gly	Gly	Ala
Pro	Leu 355	Leu	Ser	Asp	Thr	Phe	Ala 360	Ala	Gly	Phe	Met	Trp 365	Leu	Asp	Lys
Leu 370	Gly	Leu	Ser	Ala	Arg	Met 375	Gly	Ile	Glu	Val 380	Val	Met	Arg	Gln	Val
Phe 385	Phe	Gly	Ala	Gly	Asn 390	Tyr	His	Leu	Val	Asp 395	Glu	Asn	Phe	Asp	Pro 400

Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
385 390 395 400

Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
 405 410 415
 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
 420 425 430
 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
 435 440 445
 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
 450 455 460
 Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
 465 470 475 480
 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
 485 490 495
 Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
 500 505 510
 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
 515 520 525
 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
 530 535 540 543

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1721
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CT AGA GCT TTC GAC 14
 TCT CCG CTG CGC GGC AGC TGG CGG GGG GAG CAG CCA GGT GAG CCC AAG 62
 ATG CTG CTG CGC TCG AAG CCT GCG CTG CCG CCG CCG CTG ATG CTG CTG 110
 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
 5 10 15
 CTC CTG GGG CCG CTG GGT CCC CTC TCC CCT GGC GCC CTG CCC CGA CCT 158
 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
 20 25 30
 GCG CAA GCA CAG GAC GTC GTG GAC CTG GAC TTC TTC ACC CAG GAG CCG 206
 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
 35 40 45
 CTG CAC CTG GTG AGC CCC TCG TTC CTG TCC GTC ACC ATT GAC GCC AAC 254
 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
 50 55 60
 CTG GCC ACG GAC CCG CGG TTC CTC ATC CTC CTG GGT TCT CCA AAG CTT 302
 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
 65 70 75 80
 CGT ACC TTG GCC AGA GGC TTG TCT CCT GCG TAC CTG AGG TTT GGT GGC 350
 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
 85 90 95
 ACC AAG ACA GAC TTC CTA ATT TTC GAT CCC AAG AAG GAA TCA ACC TTT 398
 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
 100 105 110
 GAA GAG AGA AGT TAC TGG CAA TCT CAA GTC AAC CAG GAT ATT TGC AAA 446
 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
 115 120 125
 TAT GGA TCC ATC CCT CCT GAT GTG GAG GAG AAG TTA CGG TTG GAA TGG 494
 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
 130 135 140
 CCC TAC CAG GAG CAA TTG CTA CTC CGA GAA CAC TAC CAG AAA AAG TTC 542
 Pro Tyr Gln Glu Gln Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
 145 150 155 160
 AAG AAC AGC ACC TAC TCA AGA AGC TCT GTA GAT GTG CTA TAC ACT TTT 590

09759207.011601

Lys	Asn	Ser	Thr	Tyr	Ser	Arg	Ser	Ser	Val	Asp	Val	Leu	Tyr	Thr	Phe	
				165					170					175		
GCA	AAC	TGC	TCA	GGA	CTG	GAC	TTG	ATC	TTT	GGC	CTA	AAT	GCG	TTA	TTA	638
Ala	Asn	Cys	Ser	Gly	Leu	Asp	Leu	Ile	Phe	Gly	Leu	Asn	Ala	Leu	Leu	
				180				185					190			
AGA	ACA	GCA	GAT	TTG	CAG	TGG	AAC	AGT	TCT	AAT	GCT	CAG	TTG	CTC	CTG	686
Arg	Thr	Ala	Asp	Leu	Gln	Trp	Asn	Ser	Ser	Asn	Ala	Gln	Leu	Leu	Leu	
		195					200					205				
GAC	TAC	TGC	TCT	TCC	AAG	GGG	TAT	AAC	ATT	TCT	TGG	GAA	CTA	GGC	AAT	734
Asp	Tyr	Cys	Ser	Ser	Lys	Gly	Tyr	Asn	Ile	Ser	Trp	Glu	Leu	Gly	Asn	
	210					215					220					
GAA	CCT	AAC	AGT	TTC	CTT	AAG	AAG	GCT	GAT	ATT	TTC	ATC	AAT	GGG	TCG	782
Glu	Pro	Asn	Ser	Phe	Leu	Lys	Lys	Ala	Asp	Ile	Phe	Ile	Asn	Gly	Ser	
	225				230					235					240	
CAG	TTA	GGA	GAA	GAT	TAT	ATT	CAA	TTG	CAT	AAA	CTT	CTA	AGA	AAG	TCC	830
Gln	Leu	Gly	Glu	Asp	Tyr	Ile	Gln	Leu	His	Lys	Leu	Leu	Arg	Lys	Ser	
				245					250					255		
ACC	TTC	AAA	AAT	GCA	AAA	CTC	TAT	GGT	CCT	GAT	GTT	GGT	CAG	CCT	CGA	878
Thr	Phe	Lys	Asn	Ala	Lys	Leu	Tyr	Gly	Pro	Asp	Val	Gly	Gln	Pro	Arg	
			260					265					270			
AGA	AAG	ACG	GCT	AAG	ATG	CTG	AAG	AGC	TTC	CTG	AAG	GCT	GGT	GGA	GAA	926
Arg	Lys	Thr	Ala	Lys	Met	Leu	Lys	Ser	Phe	Leu	Lys	Ala	Gly	Gly	Glu	
		275						280				285				
GTG	ATT	GAT	TCA	GTT	ACA	TGG	CAT	CAC	TAC	TAT	TTG	AAT	GGA	CGG	ACT	974
Val	Ile	Asp	Ser	Val	Thr	Trp	His	His	Tyr	Tyr	Leu	Asn	Gly	Arg	Thr	
	290					295					300					
GCT	ACC	AGG	GAA	GAT	TTT	CTA	AAC	CCT	GAT	GTA	TTG	GAC	ATT	TTT	ATT	1022
Ala	Thr	Arg	Glu	Asp	Phe	Leu	Asn	Pro	Asp	Val	Leu	Asp	Ile	Phe	Ile	
	305				310					315					320	
TCA	TCT	GTG	CAA	AAA	GTT	TTC	CAG	GTG	GTT	GAG	AGC	ACC	AGG	CCT	GGC	1070
Ser	Ser	Val	Gln	Lys	Val	Phe	Gln	Val	Val	Glu	Ser	Thr	Arg	Pro	Gly	
				325					330					335		
AAG	AAG	GTC	TGG	TTA	GGA	GAA	ACA	AGC	TCT	GCA	TAT	GGA	GGC	GGA	GCG	1118
Lys	Lys	Val	Trp	Leu	Gly	Glu	Thr	Ser	Ser	Ala	Tyr	Gly	Gly	Gly	Ala	
		340						345					350			
CCC	TTG	CTA	TCC	GAC	ACC	TTT	GCA	GCT	GGC	TTT	ATG	TGG	CTG	GAT	AAA	1166
Pro	Leu	Leu	Ser	Asp	Thr	Phe	Ala	Ala	Gly	Phe	Met	Trp	Leu	Asp	Lys	
		355					360					365				
TTG	GGC	CTG	TCA	GCC	CGA	ATG	GGA	ATA	GAA	GTG	GTG	ATG	AGG	CAA	GTA	1214
Leu	Gly	Leu	Ser	Ala	Arg	Met	Gly	Ile	Glu	Val	Val	Met	Arg	Gln	Val	
	370					375					380					
TTC	TTT	GGA	GCA	GGA	AAC	TAC	CAT	TTA	GTG	GAT	GAA	AAC	TTC	GAT	CCT	1262
Phe	Phe	Gly	Ala	Gly	Asn	Tyr	His	Leu	Val	Asp	Glu	Asn	Phe	Asp	Pro	
	385				390					395					400	
TTA	CCT	GAT	TAT	TGG	CTA	TCT	CTT	CTG	TTC	AAG	AAA	TTG	GTG	GGC	ACC	1310
Leu	Pro	Asp	Tyr	Trp	Leu	Ser	Leu	Leu	Phe	Lys	Lys	Leu	Val	Gly	Thr	
				405					410					415		
AAG	GTG	TTA	ATG	GCA	AGC	GTG	CAA	GGT	TCA	AAG	AGA	AGG	AAG	CTT	CGA	1358
Lys	Val	Leu	Met	Ala	Ser	Val	Gln	Gly	Ser	Lys	Arg	Arg	Lys	Leu	Arg	
			420					425					430			
GTA	TAC	CTT	CAT	TGC	ACA	AAC	ACT	GAC	AAT	CCA	AGG	TAT	AAA	GAA	GGA	1406
Val	Tyr	Leu	His	Cys	Thr	Asn	Thr	Asp	Asn	Pro	Arg	Tyr	Lys	Glu	Gly	
		435					440					445				
GAT	TTA	ACT	CTG	TAT	GCC	ATA	AAC	CTC	CAT	AAC	GTC	ACC	AAG	TAC	TTG	1454
Asp	Leu	Thr	Leu	Tyr	Ala	Ile	Asn	Leu	His	Asn	Val	Thr	Lys	Tyr	Leu	
		450				455					460					
CGG	TTA	CCC	TAT	CCT	TTT	TCT	AAC	AAG	CAA	GTG	GAT	AAA	TAC	CTT	CTA	1502
Arg	Leu	Pro	Tyr	Pro	Phe	Ser	Asn	Lys	Gln	Val	Asp	Lys	Tyr	Leu	Leu	
		465			470					475					480	
AGA	CCT	TTG	GGA	CCT	CAT	GGA	TTA	CTT	TCC	AAA	TCT	GTC	CAA	CTC	AAT	1550
Arg	Pro	Leu	Gly	Pro	His	Gly	Leu	Leu	Ser	Lys	Ser	Val	Gln	Leu	Asn	

09759207 "011601

485	490	495	
GGT CTA ACT CTA AAG ATG GTG GAT GAT CAA ACC TTG CCA CCT TTA ATG 1598			
Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met			
500	505	510	
GAA AAA CCT CTC CGG CCA GGA AGT TCA CTG GGC TTG CCA GCT TTC TCA 1646			
Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser			
515	520	525	
TAT AGT TTT TTT GTG ATA AGA AAT GCC AAA GTT GCT GCT TGC ATC TGA 1694			
Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile			
530	535	540	543
AAA TAA AAT ATA CTA GTC CTG ACA CTG			1721

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
CGCATATGCA GGACGTCGTG GACCTG 26
- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
TATGATCCTC TAGTACTTCT CGAC 24
- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
TTCGATCCCA AGAAGGAATC AAC 23
- (2) INFORMATION FOR SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
GTAGTGATGC CATGTAACATG AATC 24

"01507" 0265260